

10/019566

WO 01/02431

PCT/SE00/01390

531 Rec'd PCT/...

31 DEC 2001

1

Sequence listing

<110> Got-A-Gene AB

<120> Recombinant adenovirus

<130> 2001575

<160> 16

<170> MS Word 97

<210> 1

<211> 36

<212> PRT

<213> Homo sapiens

<301> Hoppe HJ, Barlow PN, Reid KBM

<302> A parallel three stranded α -helical bundle at the nucleation site of collagen triple-helix formation

<303> FEBS Letters

<304> 344

<306> 191-195

<307> 1994

<400> 1

Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Asp Leu Gln Gly
1 5 10 15

Gln Val Gln His Ley Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val
20 25 30

Glu Leu Phe Pro Asn Gly
35

<210> 2
<211> 31
<212> PRT
<213> Homo sapiens
<301> Harbury PB, Zhang T, Kim PS, Albert T
<302> A switch between two-, three-, and four-stranded coiled coils in GCN4 leucine zipper mutants
<303> Science
<304> 262
<306> 1401-1407
<307> 1993-11-26
<400> 2

Met Lys Gln Ile Gly Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
1 5 10 15

Ile Glu Asn Gly Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

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<213> Pseudomonas aeruginosa
<301> Brinkmann U, Buchner J, Pastan I
<302> Independent domain folding of Pseudomonas exotoxin and single chain immunotoxins: Influence of interdomain connections
<303> Proc Natl Acad Sci US
<304> 89

<306> 3075-3079

<307> 1992

<400> 3

Ala Ser Gly Gly Pro Glu
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<212> PRT

<213> Homo sapiens

<301> Brinkmann U, Buchner J, Pastan I

<302> Independent domain folding of Pseudomonas exotoxin and single chain immunotoxins: Influence of interdomain connections

<303> Proc Natl Acad Sci US

<304> 89

<306> 3075-3079

<307> 1992

<400> Ala Ser Glu Gly Asn Ser Asp
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<211> 8

<212> PRT

<213> Mus musculus

<301> Brinkmann U, Buchner J, Pastan I

<302> Independent domain folding of *Pseudomonas* exotoxin and single chain immunotoxins: Influence of interdomain connections

<303> Proc Natl Acad Sci US

<304> 89

<306> 3075-3079

<307> 1992

<400> 5

Ala Ser Thr Pro Glu Pro Asp Pro
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<211> 13

<212> PRT

<213> *Staphylococcus aureus*

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Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ser Asp
1 5 10

<210> 7

<211> 11

<212> PRT

<213> *Homo sapiens*

<301> Dangl JL, Wensel TG, Morrison SL, Streyer L, Herzenberg LA and Oi T

<302> Segmental flexibility and complement fixation of genetically engineered chimeric human, rabbit and mouse antibodies

<303> EMBO Journal

<304> 7

<306> 1989

<307> 1988

<400> 7

Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly
1 5 10

<210> 8

<211> 11

<212> PRT

<213> Adenovirus type 5

<301> Stouten PFW, Sander C, Ruigrok WH, Cusack S

<302> New triple-helical model for the shaft of the adenovirus fibre

<303> Journal of molecular biology

<304> 226

<306> 1073-1084

<307> 1992

<400> 8

Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
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<210> 9
<211> 8
<212> PRT
<213> Simian virus 40
<301> Fisher-Fantuzzi L and Vesco C 8:5495-5503, 1988
<302> Cell-Dependent Efficiency of Reiterated Nuclear Signals in a Mutant Simian Virus 40 Oncoprotein Targeted to the Nucleus
<303> Molecular Cell Biology
<304> 8
<306> 5495-5503
<307> 1992
<400> 9

Asp Pro Lys Lys Lys Arg Lys Val
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<211> 119
<212> PRT
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Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val Val Glu Lys Glu
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Asp Val Thr Leu Asp Cys Val Tyr Glu Thre Arg Asp Thr Thr Tyr
20 25 30
Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu Ile
35 40 45

Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr Ser
50 55 60 65
Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr Ala
70 75 80
Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Gly Gly Val
85 90 95
Asn Asn Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg
100 105 110
Leu Met Val Lys Pro
115

<210> 11
<211> 133
<212> PRT
<213> Homo sapiens
<400> 11

Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu
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Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thre Leu Val Cys
20 25 30
Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Lys Ser Trp Trp
35 40 45
Val Asn Gly Lys Glu Val His Ser Gly Val Set Thr Asp Pro Gln Pro
50 55 60
Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
65 70 75
Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
80 85 90
Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
95 100 105 110
Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
115 120 125
Arg Ala Asp Ala Ala Ala
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<210> 12
<211> 114

<212> PRT

<213> Homo sapiens

<400> 12

Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr Ala Thr Gly
1 5 10 15
Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp Leu Ser Val
20 25 30
Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe Leu Ile His
35 40 45
Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu Glu Arg Phe
50 55 60 65
Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn Leu Ser Ser
70 75 80
Leu Glu Leu Gly Asp Ser Ala Leu Val Phe Cys Ala Ser Asn Ile Ala
85 90 95
Gly Gly Ser Tyr Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
100 105 110
Leu

<210> 13

<211> 52

<212> DNA

<213> Artificial sequence

<223> Sequence replacing the fiber gene sequence which was deleted between the NdeI restriction site in the fiber tail and the MunI site which begins at base 38 after the stop codon in the fiber. The sequence restores the NdeI and MunI sites and the wild type genome sequence between the fiber stop codon and the MunI site. In addition the added sequence contains an XhoI site allowing for the ligation of recombinant fibers.

<400> 13

tatgcactcg agtaaagaat cgtttgtgtt atgtttcaac gtgtttatttt tc

<210>	14			
<211>	1746			
<212>	DNA			
<213>	Human adenovirus type 5			
<221>	CDS			
<222>	1-1746			
<223>	1-129 Fiber tail 130-1200 Fiber shaft 1201-1746 Fiber knob			
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atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca		48		
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro				
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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc		96		
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro				
20	25	30		
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct		144		
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser				
35	40	45		
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc		192		
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu				
50	55	60		
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc		240		
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser				
65	70	75	80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac		288		
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn				
85	90	95		
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta		336		
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu				
100	105	110		
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc		384		
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr				
115	120	125		
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att		432		
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile				
130	135	140		
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa		480		
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln				
145	150	155	160	

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	
275 280 285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Ser Lys Lys Leu Glu	
305 310 315 320	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
325 330 335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
340 345 350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
355 360 365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac	1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp	
370 375 380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asp Lys Leu Thr	
385 390 395 400	
ttg tgg acc aca cca gct cca tct aac tgt aga cta aat gca gag	1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
405 410 415	

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
420 425 430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
450 455 460	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	1440
Gly Val Leu Leu Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe	
465 470 475 480	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac ggt gtt gga	1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Gly Val Gly	
485 490 495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
500 505 510	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
515 520 525	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc	1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	
545 550 555 560	
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca	1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser	
565 570 575	
tac att gcc caa gaa taa	
Tyr Ile Ala Gln Glu ***	

<210>	15
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<212>	PRT
<213>	Mus musculus
<400>	15

Asp Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Leu Gly Gly	
1 5 10 15	

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
 Tyr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Leu Val
 35 40 45
 Ala Ala Ile Asn Ser Asp Gly Gly Ile Thr Tyr Tyr Leu Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Phe Tyr Cys
 80 85 90 95
 Ala Arg His Arg Ser Gly Tyr Phe Ser Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Ser Val Thr Val Ser Ser Gly Ser
 115

<210> 16
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 <212> PRT
 <213> Mus musculus

 <400> 16

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 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Ile
 35 40 45
 Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
 65 70 75 80
 Glu Asp Leu Ala Asp Phe Phe Cys Gln Gln Tyr Ser Asn Tyr Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
 100 105 110
 Pro Thr Val Ser
 115